WEST Search History

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DATE: Wednesday, November 30, 2005

Hide?	Set Name	Query	Hit Count
	DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=OR		
☐	L1	singh.in. and anthra$	170
☐	L2	L1 and iota$	3
☐	L3	yogendra	1740
☐	L4	L3 and anthra$	156
☐	L5	L4 and iota$	3
☐	L6	iota$.clm. and (anthrax$ or anthra$).clm.	12
☐	L7	(khanna or hemant)in. and anthra$	3682
☐	L8	L7 and iota$	7
☐	L9	5,935,990.pn.	2

END OF SEARCH HISTORY

DOCUMENT-IDENTIFIER: US 20020048590 A1
TITLE: Targeting antigens to the MHC class I processing pathway with an anthrax toxin fusion protein

CLAIMS:

1. A vaccine capable of inducing an immune response in a mammal to a specific antigen wherein the vaccine comprises a unit dose of an anthrax protective antigen and said specific antigen bound to an anthrax protective antigen binding protein.

6. The vaccine of claim 1 wherein the anthrax protective antigen binding protein is the lethal factor of Bacillus anthracis.

7. The vaccine of claim 1 wherein the anthrax protective antigen binding protein comprises at least about the first 250 amino acid residues of the lethal factor of Bacillus anthracis and less than all of the amino acid residues of the lethal factor.

8. The vaccine of claim 1 wherein the molar ratio of protective antigen to the antigen bound to an anthrax protective antigen binding protein is greater than one.

9. A method of immunizing a mammal against an antigen which comprises administering a safe and effective amount of a vaccine comprising an anthrax protective antigen and said antigen bound to an anthrax protective antigen binding protein.

14. The method of claim 9 wherein the anthrax protective antigen binding protein is the lethal factor of Bacillus anthracis.

15. The method of claim 9 wherein the anthrax protective antigen binding protein comprises at least about the first 250 amino acid residues of the lethal factor of Bacillus anthracis and less than all of the amino acid residues of the lethal factor.

16. The method of claim 9 wherein the molar ratio of protective antigen to the antigen bound to an anthrax protective antigen binding protein is greater than one.

19. The method of claim 9 wherein the vaccine is administered in a unit dose that is between 10 to 500 nanograms of antigen bound to an anthrax protective antigen binding protein per kilogram of said mammal.

20. A method of inducing antigen presenting mammalian cells to present specific antigens on their cell membranes via the MHC class I processing pathway, comprising: i) selecting cells that can process and present specific antigens on their cell membranes via the MHC class I processing pathway; ii) contacting the cells with an anthrax protective antigen and said specific antigen bound to an anthrax protective antigen binding protein; and, iii) permitting the cells to internalize, process and present said specific antigen bound to an anthrax protective antigen binding protein on its cell membrane, forming a specific antigen presenting cell.

23. The method of claim 20 wherein the anthrax protective antigen binding protein is the lethal factor of Bacillus anthracis.

24. The method of claim 20 wherein the anthrax protective antigen binding protein comprises at least about the first 250 amino acid residues of the lethal factor of Bacillus anthracis and less than all of the

amino acid residues of the lethal factor.

25. The method of claim 20 wherein the molar ratio of protective antigen to the antigen bound to an anthrax protective antigen binding protein is greater than one.

27. A vaccine for inducing an immune response in a mammal to a specific antigen wherein the vaccine comprises a unit dose of a binary toxin protective antigen and the antigen bound to a binary toxin protective antigen binding protein wherein the binary toxin is selected from the group comprising iota toxin and anthrax toxin.

28. The vaccine of claim 27, wherein the binary toxin is iota toxin.

20030198651. 27 May 03. 23 Oct 03. Targeting antigens to the MHC class I processing pathway with an anthrax toxin fusion protein. Klimpel, Kurt, et al. 424/246.1; A61K039/07.

☐ 8. 20030198595. 17 May 02. 23 Oct 03. Use of bi-specific antibodies for pre-targeting diagnosis and therapy. Goldenberg, David M., et al. 424/1.49; 530/391.1 534/11 A61K051/00 C07K016/46.

☐ 9. 20030148409. 15 Oct 02. 07 Aug 03. Direct targeting binding proteins. Rossi, Edmund, et al. 435/7.23; 424/1.49 530/388.8 A61K051/00 G01N033/574 C07K016/30.

☐ 10. 20020048590. 09 May 01. 25 Apr 02. Targeting antigens to the MHC class I processing pathway with an anthrax toxin fusion protein. Klimpel, Kurt, et al. 424/246.1; A61K039/07.

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L5: Entry 1 of 4 File: PGPB Apr 25, 2002

DOCUMENT-IDENTIFIER: US 20020048590 A1
TITLE: Targeting antigens to the MHC class I processing pathway with an anthrax toxin fusion protein

CLAIMS:

27. A vaccine for inducing an immune response in a mammal to a specific antigen wherein the vaccine comprises a unit dose of a binary toxin protective antigen and the antigen bound to a binary toxin protective antigen binding protein wherein the binary toxin is selected from the group comprising iota toxin and anthrax toxin.

28. The vaccine of claim 27, wherein the binary toxin is iota toxin.

Iotab 87 3a

IDS

Sellman 2001

Svard 1997

PA-D 1988

Iotab Perelle et al 1993

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L5: Entry 2 of 4 File: USPT Apr 10, 2001

DOCUMENT-IDENTIFIER: US 6214602 B1
TITLE: Host cells for expression of clostridial toxins and proteins

CLAIMS:

3. The host cell of claim 2, wherein said clostridial proteins are selected from the group consisting of light chains of botulinal neurotoxins, heavy chains of botulinal neurotoxins, botulinal C3 protein, clostridial iota toxin Ia protein, and light and heavy chains of tetanus toxin .

AUTHORS' CORRECTIONS

Characterization of *Clostridium perfringens* Iota-Toxin Genes and Expression in *Escherichia coli*

SYLVIE PERELLE, MARYSE GIBERT, PATRICE BOQUET, AND MICHEL R. POPOFF

Laboratoire des Toxines Microbiennes, Institut Pasteur, 28 Rue du Dr. Roux, 75724 Paris Cedex 15, France

Volume 61, no. 12, p. 5147–5156: A DNA sequence mistake has been found at the end of the Ia gene. The five C-terminal amino acids of Ia are incorrect, and the Ia sequence is 67 amino acids longer. The Ia and Ib genes are separated by 40 noncoding nucleotides; the Ib sequence is not changed. The Ia sequence has been corrected in the EMBL data library and should appear as shown below:

```
  1 MKKVNKSISV FLILYLILTS SFPSYTYAQD LQIASNYITD RAFIERPEDF
 51 LKDKENAIQW EKKEAERVEK NLDTLEKEAL ELYKKDSEQI SNYSQTRQYF
101 YDYQIESNPR EKEYKNLRNA ISKNKIDKPI NVYYFESPEK FAFNKEIRTE
151 NQNEISLEKF NELKETIQDK LFKQDGFKDV SLYEPGNGDE KPTPLLIHLK
201 LPKNTGMLPY INSNDVKTLI EQDYSIKIDK IVRIVIEGKQ YIKAEASIVN
251 SLDFKDDVSK GDLWGKENYS DWSNKLTPNE LADVNDYMRG GYTAINNYLI
301 SNGPLNNPNP ELDSKVNNIE NALKLTPIPS NLIVYRRSGP QEFGLTLTSP
351 EYDFNKIENI DAFKEKWEGK VITYPNFIST SIGSVNMSAF AKRKIILRIN
401 IPKDSPGAYL SAIPGYAGEY EVLLNHGSKF KINKVDSYKD GTVTKLILDA
451 TLIN*
```

Characterization of the Structural Elements in Lipid A Required for Binding of a Recombinant Fragment of Bactericidal/Permeability-Increasing Protein $rBPI_{23}$

HÉLÈNE GAZZANO-SANTORO, JAMES B. PARENT, PAUL J. CONLON, HERBERT G. KASLER, CHAO-MING TSAI, DEBORAH A. LILL-ELGHANIAN, AND RAWLE I. HOLLINGSWORTH

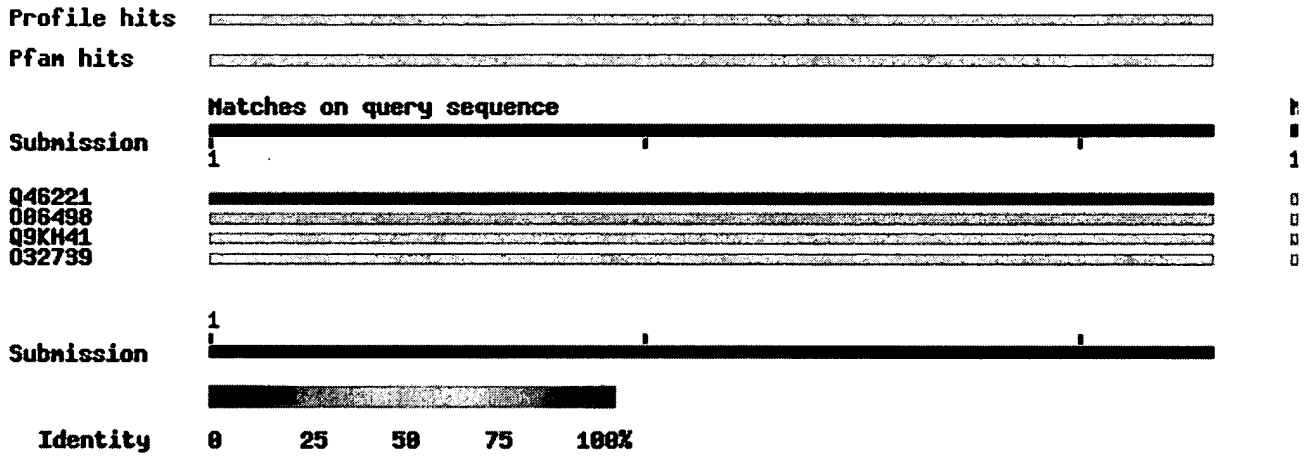
Sepsis Research Department, XOMA Corporation, Berkeley, California 94710; Neurocrine Biosciences, San Diego, California 92121; Department of Health and Human Services, Center for Biologics Evaluation and Research, Food and Drug Administration, Bethesda, Maryland 20892; and Departments of Biochemistry and Chemistry, Michigan State University, East Lansing, Michigan 48824

Volume 63, no. 6, p. 2201–2205: We failed to cite the study by Holst et al. in which the original structure of *Escherichia coli* J5 lipid A was first reported (O. Holst, S. Müller-Loennies, B. Lindner, and H. Brade, Eur. J. Biochem. **214**:695–701, 1993).

☐ tr Q9KH41 _CLODI CdtB [cdtB] [Clostridium difficile]
☐ tr O32739 _CLODI ADP-ribosyltransferase [cdtB] [Clostridium diffi

Graphical overview of the alignments

Click here to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs
(? Help) (use ScanProsite for more details about PROSITE matches)



Alignments

tr Q46221 Q46221_CLOPE **Iota toxin component Ib precursor [Clostridium perfringens]** 875 AA align

Score = 73.2 bits (165), Expect = 7e-13
Identities = 23/23 (100%), Positives = 23/23 (100%)

```
Query: 1   DANTVGVSISAGYQNGFTGNITT 23
           DANTVGVSISAGYQNGFTGNITT
Sbjct: 332 DANTVGVSISAGYQNGFTGNITT 354
```

tr O06498 O06498_9MOLU **Sb component [sbs] [Clostridium spiroforme]** 879 AA align

Score = 52.8 bits (117), Expect = 9e-07
Identities = 17/23 (73%), Positives = 17/23 (73%)

```
Query: 1   DANTVGVSISAGYQNGFTGNITT 23
```

```
            DANT GV I   YQNGFTG ITT
Sbjct: 336 DANTAGVAINIAYQNGFTGSITT 358
```

tr Q9KH41 **CdtB [cdtB] [Clostridium difficile]** 876 AA
Q9KH41_CLODI align

```
 Score = 49.8 bits (110), Expect = 7e-06
 Identities = 15/23 (65%), Positives = 18/23 (78%)

Query: 1   DANTVGVSISAGYQNGFTGNITT 23
           + NT GVS+  GYQNGFT N+TT
Sbjct: 333 ESNTAGVSVNVGYQNGFTANVTT 355
```

tr O32739 **ADP-ribosyltransferase [cdtB] [Clostridium difficile]** 876 AA
O32739_CLODI
align

```
 Score = 49.8 bits (110), Expect = 7e-06
 Identities = 15/23 (65%), Positives = 18/23 (78%)

Query: 1   DANTVGVSISAGYQNGFTGNITT 23
           + NT GVS+  GYQNGFT N+TT
Sbjct: 333 ESNTAGVSVNVGYQNGFTANVTT 355
```

```
Database: EXPASY/UniProtKB
    Posted date:  Nov 21, 2005  2:19 PM
  Number of letters in database: 854,910,163
  Number of sequences in database:  2,618,771

Lambda     K      H
   0.349    0.280     1.64

Gapped
Lambda     K      H
   0.294    0.110    0.610

Matrix: PAM30
Gap Penalties: Existence: 9, Extension: 1
Number of HSP's successfully gapped in prelim test: 0
length of query: 23
length of database: 854,910,163
```

```
effective HSP length: 14
effective length of query: 9
effective length of database: 818,247,369
effective search space: 7364226321
effective search space used: 7364226321
T: 16
A: 40
X1: 14 ( 7.0 bits)
X2: 35 (14.8 bits)
X3: 58 (24.6 bits)
S1: 40 (22.0 bits)
S2: 62 (29.5 bits)

Wallclock time: 2 seconds
```

```
CLUSTAL W (1.82) multiple sequence alignment


sp|P13423|PAG_BACAN         MKKRKVLIPLMALSTILVSSTGNLEVIQAEVKQENRLLNESESSSQGLLG
tr|Q68GS1|Q68GS1_BACAN      ---------------------------MEVKQENRLLNESESSSQGLLG
tr|Q52NH4|Q52NH4_BACAN      MKKRKVLIPLMALSTILVSSTGNLEVIQAEVKQENRLLNESESSSQGLLG
tr|Q4ZE94|Q4ZE94_BACAN      --------------------------------------------------


sp|P13423|PAG_BACAN         YYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYFQSAIWSGFIKV
tr|Q68GS1|Q68GS1_BACAN      YYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYFQSAIWSGFIKV
tr|Q52NH4|Q52NH4_BACAN      YYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYFQSAIWSGFIKV
tr|Q4ZE94|Q4ZE94_BACAN      --------------------------------------------------


sp|P13423|PAG_BACAN         KKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQYQ
tr|Q68GS1|Q68GS1_BACAN      KKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQYQ
tr|Q52NH4|Q52NH4_BACAN      KKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQYQ
tr|Q4ZE94|Q4ZE94_BACAN      --------------------------------------------------


sp|P13423|PAG_BACAN         RENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSA
tr|Q68GS1|Q68GS1_BACAN      RENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSA
tr|Q52NH4|Q52NH4_BACAN      RENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSA
tr|Q4ZE94|Q4ZE94_BACAN      --------------------------------------------------


sp|P13423|PAG_BACAN         GPTVPDRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKS
tr|Q68GS1|Q68GS1_BACAN      GPTVPDRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKS
tr|Q52NH4|Q52NH4_BACAN      GPTVPDRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKS
tr|Q4ZE94|Q4ZE94_BACAN      ---VPDRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKS
                               **********************************************


sp|P13423|PAG_BACAN         SPEKWSTASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIIL
tr|Q68GS1|Q68GS1_BACAN      SPEKWSTASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIIL
tr|Q52NH4|Q52NH4_BACAN      SPEKWSTASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIIL
tr|Q4ZE94|Q4ZE94_BACAN      SPEKWSTASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIIL
                            **************************************************


sp|P13423|PAG_BACAN         SKNEDQSTQNTDSQTRTISKNTSTSRTHTSEVHGNAEVHASFFDIGGSVS
tr|Q68GS1|Q68GS1_BACAN      SKNEDQSTQNTDSQTRTISKNTSTSRTHTSEVHGNAEVHASFFDIGGSVS
tr|Q52NH4|Q52NH4_BACAN      SKNEDQSTQNTDSQTRTISKNTSTSRTHTSEVHGNAEVHASFFDIGGSVS
tr|Q4ZE94|Q4ZE94_BACAN      SKNEDQSTQNTDSQTRTISKNTSTSRTHTSEVHGNAEVHASFFDIGGSVS
                            **************************************************


sp|P13423|PAG_BACAN         AGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARLNANIRYVNTGT
tr|Q68GS1|Q68GS1_BACAN      AGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARLNANIRYVNTGT
tr|Q52NH4|Q52NH4_BACAN      AGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARLNANIRYVNTGT
tr|Q4ZE94|Q4ZE94_BACAN      AGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARLNANIRYVNTGT
                            **************************************************


sp|P13423|PAG_BACAN         APIYNVLPTTSLVLGKNQTLATIKAKENQLSQILAPNNYYPSKNLAPIAL
tr|Q68GS1|Q68GS1_BACAN      APIYNVLPTTSLVLGKNQTLATIKAKENQLSQILAPNNYYPSKNLAPIAL
tr|Q52NH4|Q52NH4_BACAN      APIYNVLPTTSLVLGKNQTLATIKAKENQLSQILAPNNYYPSKNLAPIAL
tr|Q4ZE94|Q4ZE94_BACAN      APIYNVLPTTSLVLGKNQTLATIKAKENQLSQILAPNNYYPSKNLAPIAL
                            **************************************************


sp|P13423|PAG_BACAN         NAQDDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRV
tr|Q68GS1|Q68GS1_BACAN      NAQDDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRV
tr|Q52NH4|Q52NH4_BACAN      NAQDDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRV
```

```
tr|Q4ZE94|Q4ZE94_BACAN      NAQDDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRV
                            **************************************************

sp|P13423|PAG_BACAN         DTGSNWSEVLPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDM
tr|Q68GS1|Q68GS1_BACAN      DTGSNWSEVLPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDM
tr|Q52NH4|Q52NH4_BACAN      DTGSNWSEVLPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDM
tr|Q4ZE94|Q4ZE94_BACAN      DTGSNWSEVLPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDM
                            **************************************************

sp|P13423|PAG_BACAN         TLKEALKIAFGFNEPNGNLQYQGKDITEFDFNFDQQTSQNIKNQLAELNA
tr|Q68GS1|Q68GS1_BACAN      TLKEALKIAFGFNEPNGNLQYQGKDITEFDFNFDQQTSQNIKNQLAELNA
tr|Q52NH4|Q52NH4_BACAN      TLKEALKIAFGFNEPNGNLQYQGKDITEFDFNFDQQTSQNIKNQLAELNA
tr|Q4ZE94|Q4ZE94_BACAN      TLKEALKIAFGFNEPNGNLQYQGKDITEFDFNFDQQTSQNIKNQLAELNA
                            **************************************************

sp|P13423|PAG_BACAN         TNIYTVLDKIKLNAKMNILIRDKRFHYDRNNIAVGADESVVKEAHREVIN
tr|Q68GS1|Q68GS1_BACAN      TNIYTVLDKIKLNAKMNILIRDKRFHYDRNNIAVGADESVVKEAHREVIN
tr|Q52NH4|Q52NH4_BACAN      TNIYTVLDKIKLNAKMNILIRDKRFHYDRNNIAVGADESVVKEAHREVIN
tr|Q4ZE94|Q4ZE94_BACAN      TNIYTVLDKIKLNAKMNILIRDKRFHYDRNNIAVGADESVVKEAHREVIN
                            **************************************************

sp|P13423|PAG_BACAN         SSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRYDMLNISSLRQD
tr|Q68GS1|Q68GS1_BACAN      SSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRYDMLNISSLRQD
tr|Q52NH4|Q52NH4_BACAN      SSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRYDMLNISSLRQD
tr|Q4ZE94|Q4ZE94_BACAN      SSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRYDMLNISSLRQD
                            **************************************************

sp|P13423|PAG_BACAN         GKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNGI
tr|Q68GS1|Q68GS1_BACAN      GKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNGI
tr|Q52NH4|Q52NH4_BACAN      GKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNGI
tr|Q4ZE94|Q4ZE94_BACAN      GKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNGI
                            **************************************************

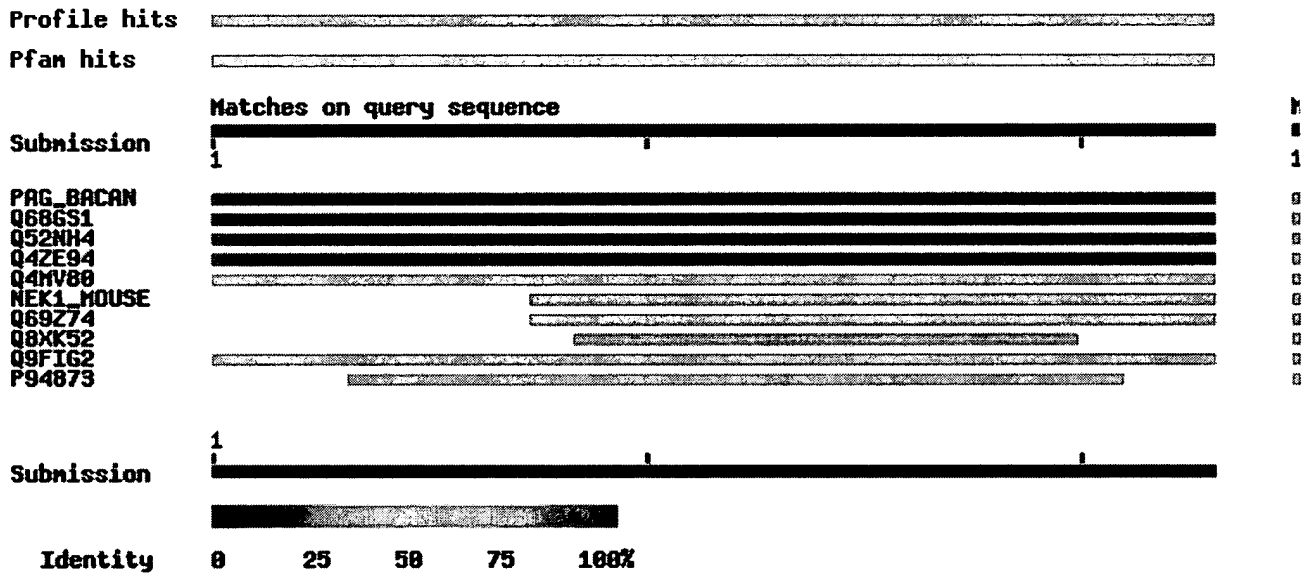
sp|P13423|PAG_BACAN         KKILIFSKKGYEIG
tr|Q68GS1|Q68GS1_BACAN      KKILIFSKKGYEIG
tr|Q52NH4|Q52NH4_BACAN      KKILIFSKKGYEIG
tr|Q4ZE94|Q4ZE94_BACAN      KKILIFSKKGYEIG
                            **************
```

- [x] sp P13423 PAG_BACAN Protective antigen precursor (PA) (PA-83) (P.
- [x] tr Q68GS1 _BACAN Protective antigen [Bacillus anthracis]
- [x] tr Q52NH4 _BACAN Protective antigen [pag] [Bacillus anthracis]
- [x] tr Q4ZE94 _BACAN Protective antigen (Fragment) [pa] [Bacillus ant
- [ ] tr Q4MV80 _BACCE Protective antigen [BCE_G9241_pBC218_0026] [Baci
- [ ] sp P51954 NEK1_MOUSE Serine/threonine-protein kinase Nek1 (EC 2..
- [ ] tr Q69Z74 _MOUSE MKIAA1901 protein (Fragment) [Nek1] [Mus musculu
- [ ] tr Q8XK52 _CLOPE Probable endo-1,4-beta-xylanase [CPE1551] [Clost
- [ ] tr Q9FIG2 _ARATH Serine protease-like protein (Hypothetical prote
- [ ] tr P94873 _LYSLA Alpha-aminoadipyl-cysteinyl-valine synthetase [p

Graphical overview of the alignments

Click here to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs

(? Help) (use ScanProsite for more details about PROSITE matches)



Alignments

sp	P13423 PAG_BACAN	**Protective antigen precursor (PA) (PA-83) (PA83) (Anthrax toxins translocating protein) [Contains: Protective antigen PA-20 (PA20); Protective antigen PA-63 (PA63)] [pagA] [Bacillus anthracis]**	764 AA align

Score = 74.4 bits (168), Expect = 3e-13
Identities = 23/23 (100%), Positives = 23/23 (100%)

```
Query: 1   THTSEVHGNAEVHASFFDIGGSV 23
           THTSEVHGNAEVHASFFDIGGSV
Sbjct: 327 THTSEVHGNAEVHASFFDIGGSV 349
```

tr Q68GS1 **Protective antigen [Bacillus anthracis]** 736 AA
Q68GS1_BACAN

align

Score = 74.4 bits (168), Expect = 3e-13
Identities = 23/23 (100%), Positives = 23/23 (100%)

```
Query: 1   THTSEVHGNAEVHASFFDIGGSV 23
           THTSEVHGNAEVHASFFDIGGSV
Sbjct: 299 THTSEVHGNAEVHASFFDIGGSV 321
```

tr Q52NH4 **Protective antigen [pag] [Bacillus anthracis]** 764 AA
Q52NH4_BACAN

align

Score = 74.4 bits (168), Expect = 3e-13
Identities = 23/23 (100%), Positives = 23/23 (100%)

```
Query: 1   THTSEVHGNAEVHASFFDIGGSV 23
           THTSEVHGNAEVHASFFDIGGSV
Sbjct: 327 THTSEVHGNAEVHASFFDIGGSV 349
```

tr Q4ZE94 **Protective antigen (Fragment) [pa] [Bacillus anthracis]** 561 AA
Q4ZE94_BACAN

align

Score = 74.4 bits (168), Expect = 3e-13
Identities = 23/23 (100%), Positives = 23/23 (100%)

```
Query: 1   THTSEVHGNAEVHASFFDIGGSV 23
           THTSEVHGNAEVHASFFDIGGSV
Sbjct: 124 THTSEVHGNAEVHASFFDIGGSV 146
```

```
CLUSTAL W (1.81) multiple sequence alignment

unk|VIRT2310|Blast_submission      ------------------------------------------------
tr|Q46221|Q46221_CLOPE             MNIQIKNVFSFLTLTAMISQTLSYNVYAQTTTQNDTNQKEEITNENTLS

unk|VIRT2310|Blast_submission      ------------------------------------------------
tr|Q46221|Q46221_CLOPE             NGLMGYYFADEHFKDLELMAPIKNGDLKFEEKKVDKLLTEDNSSIKSIR

unk|VIRT2310|Blast_submission      ------------------------------------------------
tr|Q46221|Q46221_CLOPE             TGRIIPSEDGEYILSTDRNDVLMQINAKGDIAKTLKVNMKKGQAYNIRI

unk|VIRT2310|Blast_submission      ------------------------------------------------
tr|Q46221|Q46221_CLOPE             IQDKNLGSIDNLSVPKLYWELNGNKTVIPEENLFFRDYSKIDENDPFIP

unk|VIRT2310|Blast_submission      ------------------------------------------------
tr|Q46221|Q46221_CLOPE             NNFFDVRFFSAAWEDEDLDTDNDNIPDAYEKNGYTIKDSIAVKWNDSFA

unk|VIRT2310|Blast_submission      ------------------------------------------------
tr|Q46221|Q46221_CLOPE             QGYKKYVSSYLESNTAGDPYTDYQKASGSIDKAIKLEARDPLVAAYPVV

unk|VIRT2310|Blast_submission      -------------------------------DANTVGVSISAGYQNGFT
tr|Q46221|Q46221_CLOPE             VGMENLIISTNEHASSDQGKTVSRATTNSKTDANTVGVSISAGYQNGFT
                                                 ******************

unk|VIRT2310|Blast_submission      NITT--------------------------------------------
tr|Q46221|Q46221_CLOPE             NITTSYSHTTDNSTAVQDSNGESWNTGLSINKGESAYINANVRYYNTGT
                                   ****

unk|VIRT2310|Blast_submission      ------------------------------------------------
tr|Q46221|Q46221_CLOPE             PMYKVTPTTNLVLDGETLATIKAQDNQIGNNLSPNETYPKKGLSPLALN

unk|VIRT2310|Blast_submission      ------------------------------------------------
tr|Q46221|Q46221_CLOPE             MDQFNARLIPINYDQLKKLDSGKQIKLETTQVSGNYGTKNSQGQIITEG

unk|VIRT2310|Blast_submission      ------------------------------------------------
tr|Q46221|Q46221_CLOPE             SWSNYISQIDSVSASIILDTGSQTFERRVAAKEQGNPEDKTPEITIGEA

unk|VIRT2310|Blast_submission      ------------------------------------------------
tr|Q46221|Q46221_CLOPE             KKAFSATKNGELLYFNGIPIDESCVELIFDDNTSEIIKEQLKYLDDKKI

unk|VIRT2310|Blast_submission      ------------------------------------------------
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unk|VIRT2310|Blast_submission      ------------------------------------------------
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unk|VIRT2310|Blast_submission   -------------------------
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Welcome to the SIB BLAST Network Service

If results of this search are reported or published, please mention t
the computation was performed at the SIB using the BLAST network ser
The SIB BLAST network service uses a server developed at SIB and the
BLAST 2 software.

In case of problems, please read the online BLAST help.
If your question is not covered, please contact <helpdesk@expasy.org>

NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Mille
Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein
database search programs. Nucleic Acids Res. 25:3389-3402(1997).

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Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]
Database: EXPASY/UniProtKB
2,618,771 sequences; 854,910,163 total letters
UniProt Knowledgebase Release 6.5 consists of:
UniProtKB/Swiss-Prot Release 48.5 of 22-Nov-2005: 199607 entries
UniProtKB/TrEMBL Release 31.5 of 22-Nov-2005: 2406391 entries

Taxonomic view | NiceBlast view | Printable view

List of potentially matching sequences

Send selected sequences to
Clustal W (multiple alignment) Submit Query
Select up to...

☐ Include query sequence

Db AC Description

☐ tr Q46221 _CLOPE Iota toxin component Ib precursor [Clostridium p
☐ tr O06498 _9MOLU Sb component [sbs] [Clostridium spiroforme]

EBI **Dbfetch**

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DT   18-APR-2005 (Rel. 83, Last updated, Version 15)
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OC   Clostridium.
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RX   PUBMED; 8225592.
RA   Perelle S., Gibert M., Boquet P., Popoff M.R.;
RT   "Characterization of Clostridium perfringens iota toxin genes and
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RL   Infect. Immun. 61(12):5147-5156(1993).
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RC   revised by [3]   MAT
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RT   ;
RL   Submitted (30-APR-1993) to the EMBL/GenBank/DDBJ databases.
RL   M.R. Popoff, Institut Pasteur, 28 rue du Dr. Roux, Toxines Microbiennes,
RL   75015 Paris Cedex 15, FRANCE
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RL   75015 Paris Cedex 15, FRANCE
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UniProtKB/TrEMBL entry Q46221

Printer-friendly view Request update

[Entry info] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name	**Q46221_CLOPE**
Primary accession number	**Q46221**
Secondary accession numbers	None
Entered in TrEMBL in	Release 01, November 1996
Sequence was last modified in	Release 01, November 1996
Annotations were last modified in	Release 24, June 2003

Name and origin of the protein

Protein name	**Iota toxin component Ib [Precursor]**
Synonyms	None
Gene name	None
From	Clostridium perfringens [TaxID: 1502]
Taxonomy	Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiace Clostridium.

References

[1] NUCLEOTIDE SEQUENCE.
STRAIN=NCIB 10748;
PubMed=8225592 [NCBI, ExPASy, EBI, Israel, Japan]
Perelle S., Gibert M., Boquet P., Popoff M.R.;
"Characterization of Clostridium perfringens iota toxin genes and expression in Escherichi coli.";
Infect. Immun. 61:5147-5156(1993).

[2] NUCLEOTIDE SEQUENCE.
STRAIN=NCIB 10748;
Popoff M.R.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.

Comments

None

Cross-references

EMBL	X73562; CAA51960.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	I40862; I40862.	
HSSP	P13423; 1ACC. [HSSP ENTRY / PDB]	

GO	GO:0005576; Cellular component: extracellular region *(inferred from electrc annotation).* GO:0009405; Biological process: pathogenesis *(inferred from electronic annotation).* QuickGo view.
InterPro	IPR003896; Anthrax_toxinB. IPR011658; PA14. Graphical view of domain structure.
Pfam	PF03495; Binary_toxB; 1. PF07691; PA14; 1. Pfam graphical view of domain structure.
PRINTS	PR01391; BINARYTOXINB.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOGENOM	[Family / Alignment / Tree]
ProtoMap	Q46221.
PRESAGE	Q46221.
ModBase	Q46221.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% / 100% identity.

Keywords

Signal.

Features

 Feature table viewer

Key	From	To	Length	Description
SIGNAL	34	39	6	*Potential.*
CHAIN	212	875	664	iota toxin component Ib.

Sequence information

Length: **875 AA** [This is the length of the unprocessed precursor]

Molecular weight: **98469 Da** [This is the MW of the unprocessed precursor]

CRC64: **C9AE092CD3818921** is a checksum on the sequenc

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BLAST submission on ExPASy/SIB or at NCBI (USA)

Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

ScanProsite, MotifScan

Submit a homology modeling request to SWISS-MODEL

NPSA Sequence analysis tools

☐ **1:** X73562. Reports C.perfringens DNA...[gi:929031] Links

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LOCUS       CPITOXIAB               5745 bp    DNA     linear   BCT 18-APR-2005
DEFINITION  C.perfringens DNA for iota toxin polypeptides Ia and Ib.
ACCESSION   X73562
VERSION     X73562.1  GI:929031
KEYWORDS    iota toxin; iota toxin Ia; iota toxin Ib.
SOURCE      Clostridium perfringens
  ORGANISM  Clostridium perfringens
            Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
            Clostridium.
REFERENCE   1
  AUTHORS   Perelle,S., Gibert,M., Boquet,P. and Popoff,M.R.
  TITLE     Characterization of Clostridium perfringens iota-toxin genes and
            expression in Escherichia coli
  JOURNAL   Infect. Immun. 61 (12), 5147-5156 (1993)
   PUBMED   8225592
REFERENCE   2
  AUTHORS   Popoff,M.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-APR-1993) M.R. Popoff, Institut Pasteur, 28 rue du
            Dr. Roux, Toxines Microbiennes, 75015 Paris Cedex 15, FRANCE
  REMARK    revised by [3]   MAT
REFERENCE   3  (bases 1 to 5745)
  AUTHORS   Popoff,M.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-AUG-1995) M.R. Popoff, Institut Pasteur, 28 rue du
            Dr. Roux, Toxines Microbiennes, 75015 Paris Cedex 15, FRANCE
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Go to: General Description References Additional Sequence

General Information

Primary Accession #	X73562
Accession #	X73562
Entry Name	EMBL:CPITOXIAB
Molecule Type	genomic DNA
Sequence Length	5745
Entry Division	PRO
Sequence Version	X73562.1
Creation Date	04-NOV-1993
Modification Date	18-APR-2005

Description

Description	C.perfringens DNA for iota toxin polypeptides Ia and Ib
Keywords	iota toxin; iota toxin Ia; iota toxin Ib.;
Organism	Clostridium perfringens
Organism Classification	Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.

References

1. Perelle,S.; Gibert,M.; Boquet,P.; Popoff,M.R.;
Characterization of Clostridium perfringens iota toxin gene expression in Escherichia coli
Infect. Immun. 61(12):5147-5156 (1993)
Pubmed 8225592

2. Popoff,M.R.; Submitted (30-APR-1993) to the EMBL/GenBank/DDBJ databases.
Popoff, Institut Pasteur, 28 rue du Dr. Roux, Toxines Microbiennes, 75015 Paris C
FRANCE

3. Popoff,M.R.; Submitted (03-AUG-1995) to the EMBL/GenBank/DDBJ databases
Popoff, Institut Pasteur, 28 rue du Dr. Roux, Toxines Microbiennes, 75015 Paris C
FRANCE
Position 1-5745

Additional Information

Features

Key	Location	Qualifier	Value
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		mol_type	genomic DNA
		organism	Clostridium perfringens

sub_species type E

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Go to: General Description References Additional Sequence

First Hit Fwd Refs Previous Doc Next Doc Go to Doc#

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L2: Entry 2 of 25 File: USPT Jul 15, 2003

DOCUMENT-IDENTIFIER: US 6592872 B1
TITLE: Targeting antigens to the MHC class I processing pathway with an anthrax toxin fusion protein

Brief Summary Text (97):
In general, for cloning and expression of PA, the same methods as described for antigen-APABP can be used by one skilled in the art. Genes that encode wild type or mutated proteins can be cloned and expressed by methods known to those skilled in the art, as described above. For example, the gene encoding protein Ib of the Clostridium perfringens iota toxin can be cloned and expressed for use in the present invention according the methods described herein, or by methods known to those skilled in the art. The present invention uses an isolated nucleic acid in expression vector pYS5 that encodes the PA protein, as described in Example 2.

Other Reference Publication (4):
Sirard, Jean-Claude, et al. (1997) "A Recombinant Bacillus anthracis Strain Producing the Clostridium perfringens Ib Component Induces Protection against Iota Toxins", Infection and Immunity, 65(6): 2029-2033.

Previous Doc Next Doc Go to Doc#

L2: Entry 2 of 25 File: USPT Jul 15, 2003

DOCUMENT-IDENTIFIER: US 6592872 B1
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GenCore version 5.1.6

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62.476 Million cell updates/sec

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Maximum DB seq length: 2000000000

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Maximum Match 100%
Listing first 45 summaries

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4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	101	86.3	875	2	Q46221	Q46221 clostridium
2	79	67.5	876	2	O32739	O32739 clostridium
3	79	67.5	876	2	Q9KH41	Q9kh41 clostridium
4	72	61.5	879	2	O06498	O06498 clostridium
5	54	46.2	551	16	Q8XAQ0	Q8xaq0 escherichia
6	54	46.2	551	16	Q8FBP5	Q8fbp5 escherichia
7	52	44.4	360	11	Q8K0A4	Q8k0a4 mus musculu
8	52	44.4	362	3	Q9HEZ9	Q9hez9 emericella
9	52	44.4	538	16	Q8U730	Q8u730 agrobacteri
10	52	44.4	852	11	Q8BZG1	Q8bzg1 mus musculu
11	51	43.6	689	11	Q8BSK0	Q8bsk0 mus musculu
12	51	43.6	804	11	Q99NC2	Q99nc2 mus musculu
13	51	43.6	906	11	Q99PM5	Q99pm5 mus musculu
14	51	43.6	965	11	Q99PW2	Q99pw2 mus musculu
15	51	43.6	1160	11	Q9WUN1	Q9wun1 mus musculu
16	51	43.6	1160	11	Q8R564	Q8r564 mus musculu
17	51	43.6	1198	11	Q99PM6	Q99pm6 mus musculu
18	51	43.6	1198	11	Q924G8	Q924g8 mus musculu
19	51	43.6	1987	11	Q99PB3	Q99pb3 mus musculu
20	51	43.6	3600	10	Q9SA64	Q9sa64 arabidopsis
21	50.5	43.2	434	16	Q983K6	Q983k6 rhizobium l
22	50	42.7	129	16	Q8YQU6	Q8yqu6 anabaena sp
23	50	42.7	528	3	P87239	P87239 schizosacch
24	50	42.7	537	16	Q8FIZ4	Q8fiz4 escherichia
25	50	42.7	1341	16	Q8UAU1	Q8uau1 agrobacteri
26	49	41.9	357	16	Q9KU34	Q9ku34 vibrio chol
27	49	41.9	482	11	Q8BU52	Q8bu52 mus musculu
28	48.5	41.5	228	17	Q8PWM4	Q8pwm4 methanosarc
29	48	41.0	114	2	Q9RHG4	Q9rhg4 microcystis
30	48	41.0	160	4	Q8NC35	Q8nc35 homo sapien
31	48	41.0	228	11	Q8C0L2	Q8c0l2 mus musculu
32	48	41.0	253	16	Q8ZQC5	Q8zqc5 salmonella
33	48	41.0	253	16	Q8Z804	Q8z804 salmonella
34	48	41.0	315	2	Q9X588	Q9x588 neisseria f
35	48	41.0	381	11	Q8BX42	Q8bx42 mus musculu
36	48	41.0	537	5	Q9Y154	Q9y154 drosophila
37	48	41.0	545	5	Q9VA35	Q9va35 drosophila
38	48	41.0	653	4	Q96JN4	Q96jn4 homo sapien
39	48	41.0	663	2	Q8RR60	Q8rr60 rhizobium s
40	48	41.0	727	4	Q9UDR4	Q9udr4 homo sapien
41	48	41.0	835	4	Q9ULF5	Q9ulf5 homo sapien
42	48	41.0	1323	2	O87018	O87018 helicobacte
43	48	41.0	1452	4	Q9H4A0	Q9h4a0 homo sapien
44	48	41.0	1512	4	Q9H4A1	Q9h4a1 homo sapien
45	47.5	40.6	3659	16	Q98LN6	Q98ln6 rhizobium l

ALIGNMENTS

RESULT 1
Q46221
ID Q46221 PRELIMINARY; PRT; 875 AA.
AC Q46221;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Iota toxin component Ib precursor.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIB 10748;
RX MEDLINE=94041637; PubMed=8225592;
RA Perelle S., Gibert M., Boquet P., Popoff M.R.;
RT "Characterization of Clostridium perfringens iota toxin genes and
RT expression in Escherichia coli.";
RL Infect. Immun. 61:5147-5156(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIB 10748;
RA Popoff M.R.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
DR EMBL; X73562; CAA51960.1; -.
DR HSSP; P13423; 1ACC.
DR InterPro; IPR003896; Anthrax_toxinB.
DR Pfam; PF03495; Binary_toxB; 1.
DR PRINTS; PR01391; BINARYTOXINB.
KW Signal.
FT SIGNAL 34 38 POTENTIAL.
FT CHAIN 212 875 IOTA TOXIN COMPONENT IB.
SQ SEQUENCE 875 AA; 98468 MW; C9AE092CD3818921 CRC64;

Query Match 86.3%; Score 101; DB 2; Length 875;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Infect. Immun., 12 1993, 5147-5156, Vol 61, No. 12

Characterization of Clostridium perfringens iota-toxin genes and expression in Escherichia coli [published erratum appears in Infect Immun 1995 Dec;63(12):4967]

S Perelle, M Gibert, P Boquet and MR Popoff

Laboratoire des Toxines Microbiennes, Institut Pasteur, Paris, France.

The iota toxin which is produced by Clostridium perfringens type E, is a binary toxin consisting of two independent polypeptides: Ia, which is an ADP-ribosyltransferase, and Ib, which is involved in the binding and internalization of the toxin into the cell. Two degenerate oligonucleotide probes deduced from partial amino acid sequence of each component of C. spiroforme toxin, which is closely related to the iota toxin, were used to clone three overlapping DNA fragments containing the iota-toxin genes from C. perfringens type E plasmid DNA. Two genes, in the same orientation, coding for Ia (387 amino acids) and Ib (875 amino acids) and separated by 243 noncoding nucleotides were identified. A predicted signal peptide was found for each component, and the secreted Ib displays two domains, the propeptide (172 amino acids) and the mature protein (664 amino acids). The Ia gene has

been expressed in Escherichia coli and C. perfringens, under the control of its own promoter. The recombinant polypeptide obtained was recognized by Ia antibodies and ADP-ribosylated actin. The expression of the Ib gene was obtained in E. coli harboring a recombinant plasmid encompassing the putative promoter upstream of the Ia gene and the Ia and Ib genes. Two residues which have been found to be involved in the NAD+ binding site of diphtheria and pseudomonas toxins are conserved in the predicted Ia sequence (Glu-14 and Trp-19). The predicted amino acid Ib sequence shows 33.9% identity with and 54.4% similarity to the protective antigen of the anthrax toxin complex. In particular, the central region of Ib, which contains a predicted transmembrane segment (Leu-292 to Ser-308), presents 45% identity with the corresponding protective antigen sequence which is involved in the translocation of the toxin across the cell membrane.

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